

## WEST Search History





DATE: Wednesday, May 25, 2005

<u>Hide?</u>	<u>Set Name</u>	<u>Query</u>	<u>Hit Count</u>
	<i>DB=PGPB,USPT,EPAB; PLUR=YES; OP=ADJ</i>		
<input type="checkbox"/>	L32	l8 and l30	5
<input type="checkbox"/>	L31	L30 and l21	33
<input type="checkbox"/>	L30	(514/2)![CCLS]	6636
<input type="checkbox"/>	L29	(514)![CCLS]	0
<input type="checkbox"/>	L28	20020119129.pn.	1
<input type="checkbox"/>	L27	6093565.pn.	1
<input type="checkbox"/>	L26	6242587.pn.	1
<input type="checkbox"/>	L25	L24 and L17	6
<input type="checkbox"/>	L24	L23 or L9	154
<input type="checkbox"/>	L23	L4.ti.	38
<input type="checkbox"/>	L22	L9 and L17	6
<input type="checkbox"/>	L21	L20 and L17	6570
<input type="checkbox"/>	L20	cnB or (CN with beta) or (cn with B) canB or (can with b)	408983
<input type="checkbox"/>	L19	cnB or (CN with beta) or canB or (can with b)	409019
<input type="checkbox"/>	L18	L17 and L4	242
<input type="checkbox"/>	L17	L12 or L13 or L14 or L15 or L16	62432
<input type="checkbox"/>	L16	chen.in.	43635
<input type="checkbox"/>	L15	lian.in.	690
<input type="checkbox"/>	L14	gao.in.	2563
<input type="checkbox"/>	L13	yan.in.	4377
<input type="checkbox"/>	L12	wei.in.	14630
<input type="checkbox"/>	L11	L10 not @ay>1998	19
<input type="checkbox"/>	L10	L9 and L5	82
<input type="checkbox"/>	L9	L7 or L8	154
<input type="checkbox"/>	L8	L4.ab.	79
<input type="checkbox"/>	L7	L4.clm.	107
<input type="checkbox"/>	L6	L5 and L4	1121
<input type="checkbox"/>	L5	cancer\$ or tumor\$ or neoplas\$	163081
<input type="checkbox"/>	L4	calcineurin	1464
<input type="checkbox"/>	L3	L2 or L1	2
<input type="checkbox"/>	L2	6093565.pn.	1

☐ L1 6242587.pn.

1

END OF SEARCH HISTORY

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OM protein - protein search, using sw model

Run on: April 27, 2005, 09:03:38 ; Search time 71 Seconds  
(without alignments)  
920.599 Million cell updates/sec

Title: US-09-763-720-1  
Perfect score: 870  
Sequence: 1 GNEASYPLEMCSHFDADEIK.....EEFCVVGGGLDIHKKMVVDV 169

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	870	100.0	169	7	ADE55926	Ade55926 Rat Prote
2	870	100.0	169	7	ADE55928	Ade55928 Human Pro
3	870	100.0	170	2	AAW64200	Aaw64200 Human cal
4	870	100.0	170	3	AAB09978	Aab09978 Human HCN
5	870	100.0	170	8	ADI27357	Adi27357 Human cal
6	762	87.6	170	4	ABB60493	Abb60493 Drosophil
7	739	84.9	162	4	ABB65554	Abb65554 Drosophil
8	733	84.3	170	4	AAO14411	Aao14411 Calcineur
9	733	84.3	173	4	AAB64410	Aab64410 Amino aci

10	733	84.3	173	6	ADA55632	Ada55632	Human	pro
11	733	84.3	187	4	AAU87327	Aau87327	Novel	cen
12	733	84.3	187	8	ADI54642	Adi54642	Novel	hum
13	733	84.3	189	4	AAM95239	Aam95239	Human	rep
14	733	84.3	189	4	AAM43639	Aam43639	Human	pol
15	733	84.3	189	4	AAM43564	Aam43564	Human	pol
16	733	84.3	189	4	AAU19951	Aau19951	Novel	hum
17	733	84.3	189	4	ABB95936	Abb95936	Human	tes
18	733	84.3	189	4	AAU87615	Aau87615	Novel	cen
19	733	84.3	189	8	ADI54930	Adi54930	Novel	hum
20	733	84.3	189	8	ADM24660	Adm24660	Human	PRO
21	733	84.3	189	8	ADM24585	Adm24585	Human	PRO
22	728	83.7	170	3	AAB09977	Aab09977	Human	CNB
23	501	57.6	197	8	ADS24073	Ads24073	Bacterial	
24	496	57.0	175	2	AAU00881	Aay00881	Calcineur	
25	496	57.0	175	8	ADS43790	Ads43790	Bacterial	
26	429.5	49.4	195	8	ADS44352	Ads44352	Bacterial	
27	429	49.3	185	8	ADN21422	Adn21422	Bacterial	
28	393	45.2	90	3	AAG02990	Aag02990	Human	sec
29	373.5	42.9	178	3	AAU77951	Aay77951	A. thalia	
30	340.5	39.1	195	6	ABG74662	Abg74662	Murine Ca	
31	337.5	38.8	194	6	ABG74856	Abg74856	Human cal	
32	337.5	38.8	194	7	ADD46021	Add46021	Human Pro	
33	337.5	38.8	194	7	ADE59921	Ade59921	Human Pro	
34	337.5	38.8	194	7	ADE61228	Ade61228	Human Pro	
35	337.5	38.8	194	7	ADE59917	Ade59917	Human Pro	
36	337.5	38.8	195	6	ABG74661	Abg74661	Human Ca2	
37	337.5	38.8	195	6	ABU89717	Abu89717	Protein d	
38	321.5	37.0	189	4	ABB58936	Abb58936	Drosophil	
39	316.5	36.4	213	8	ADN23634	Adn23634	Bacterial	
40	303.5	34.9	195	8	ADN23801	Adn23801	Bacterial	
41	292	33.6	207	4	AAM43642	Aam43642	Human pol	
42	292	33.6	207	4	AAU19948	Aau19948	Novel hum	
43	292	33.6	207	4	AAU87620	Aau87620	Novel cen	
44	292	33.6	207	8	ADI54935	Adi54935	Novel hum	
45	292	33.6	207	8	ADM24663	Adm24663	Human PRO	

# RESULT 3

AAW64200

ID AAW64200 standard; protein; 170 AA.

XX

AC AAW64200;

XX

DT 09-NOV-1998 (first entry)

XX

DE Human calcineurin.

XX

KW Calcineurin; interferon receptor 1 binding protein; IR1B1; human.

XX

OS Homo sapiens.

XX

PN WO9831796-A1.

XX

PD 23-JUL-1998.

XX

PF 15-JAN-1998; 98WO-US000671.

XX  
 PR 15-JAN-1997; 97US-0035636P.  
 XX  
 PA (YEDA ) YEDA RES & DEV CO LTD.  
 PA (MCIN/) MCINNIS P A.  
 XX  
 PI Revel M, Abramovitch C, Chebath JE;  
 XX  
 DR WPI; 1998-414096/35.  
 XX  
 PT New isolated interferon receptor binding proteins - used to develop  
 PT products for modulating sensitivity to interferon, e.g. in the treatment  
 PT of tumours or for prolonging graft survival.  
 XX  
 PS Example 2; Page 35-36; 64pp; English.  
 XX  
 CC This polypeptide comprises the human calcium-binding protein, calcineurin  
 CC -beta. A novel interferon receptor binding protein, IR1B1 (see AAW64199),  
 CC of the invention shows marked homology, e.g. calcium binding sites (E-F  
 CC handles), to calcineurin-beta; amino acid residues 50-171 show 59.8%  
 CC similarity and 32.5% identity. IR1B1 polypeptides and polynucleotides can  
 CC be used to develop products for modulating sensitivity to interferon,  
 CC e.g. in cancer therapy and for prolonging graft survival  
 XX  
 SQ Sequence 170 AA;

Query Match 100.0%; Score 870; DB 2; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 7.9e-83;  
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNEASYPLEMCSHFDADEIKRLGKRFKKLDLDNSGSLSVVEEFMSLPELQQNPLVQRVIDI 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2 GNEASYPLEMCSHFDADEIKRLGKRFKKLDLDNSGSLSVVEEFMSLPELQQNPLVQRVIDI 61  
 Qy 61 FDTDGNGEVDFKEFIEGVSQFSVKGDKQKLRFAFRIYDMKDGYSINGELFQVLKMMVG 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 62 FDTDGNGEVDFKEFIEGVSQFSVKGDKQKLRFAFRIYDMKDGYSINGELFQVLKMMVG 121  
 Qy 121>NNLKDTQLQQIVDKTIINADKDGGRISFEEFCAVVGGLDIHKKMVVDV 169  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 122>NNLKDTQLQQIVDKTIINADKDGGRISFEEFCAVVGGLDIHKKMVVDV 170

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OM protein - protein search, using sw model

Run on: April 27, 2005, 09:04:17 ; Search time 39 Seconds  
(without alignments)  
416.939 Million cell updates/sec

Title: US-09-763-720-1  
Perfect score: 870  
Sequence: 1 GNEASYPLEMCSHFDADEIK.....EEFCAVVGGLDIHKMVDV 169

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pirl:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	%		Query		DB	ID	Description
	Score	Match	Length				
1	870	100.0	170	1	A33391	calcineurin regula	
2	870	100.0	170	1	S34127	calcineurin regula	
3	870	100.0	216	1	S42716	calcineurin regula	
4	865	99.4	170	1	JC1220	calcineurin regula	
5	784	90.1	170	2	JC7242	calcineurin regula	
6	766	88.0	170	2	JC5174	calcineurin regula	
7	762	87.6	170	2	A44307	calcineurin regula	
8	704	80.9	369	2	T22708	hypothetical prote	
9	702	80.7	179	2	JC1221	calcineurin regula	
10	699	80.3	176	2	JQ1232	calcineurin regula	
11	620	71.3	165	2	PS0261	calcineurin regula	
12	528	60.7	174	2	T47245	calcineurin regula	
13	496	57.0	175	2	JH0462	phosphoprotein pho	

14	483	55.5	174	2	T41632	probable calcineur
15	316.5	36.4	213	2	T31775	hypothetical prote
16	303.5	34.9	195	2	T28047	hypothetical prote
17	255	29.3	311	2	T21563	hypothetical prote
18	233.5	26.8	150	2	T07122	calmodulin CAM5 -
19	233.5	26.8	151	2	A71409	calmodulin 8 [impo
20	230	26.4	591	2	S54788	calcium-stimulated
21	229.5	26.4	149	2	S35187	calmodulin 6 - Ara
22	228.5	26.3	149	1	S53006	calmodulin - leaf
23	228.5	26.3	149	1	MCPZDC	calmodulin - carro
24	228.5	26.3	149	1	S22503	calmodulin [simila
25	228.5	26.3	149	1	S22971	calmodulin - trump
26	228.5	26.3	149	1	S40301	calmodulin - red b
27	228.5	26.3	149	1	S70768	calmodulin CAM81 -
28	228.5	26.3	149	2	T47417	calmodulin 7 [simi
29	228.5	26.3	149	2	H84667	calmodulin (cam2)
30	227.5	26.1	149	1	MCBH	calmodulin - barle
31	227.5	26.1	149	1	MCWT	calmodulin - wheat
32	227.5	26.1	149	2	S24952	calmodulin 1 (clon
33	226.5	26.0	149	2	S58311	calmodulin - Biden
34	226.5	26.0	149	2	S60237	calmodulin PCM2/PC
35	225.5	25.9	149	1	MCZQF	calmodulin - malar
36	224.5	25.8	149	1	MCAA	calmodulin - alfal
37	224.5	25.8	149	2	S22860	calmodulin 2 (clon
38	223.5	25.7	149	1	I51202	calmodulin - duck
39	223.5	25.7	149	1	MCCH	calmodulin - chick
40	223.5	25.7	149	1	MCEE	calmodulin - elect
41	223.5	25.7	149	1	MCHU	calmodulin [valida
42	223.5	25.7	149	1	MCRT	calmodulin [valida
43	223.5	25.7	149	2	JC1305	calmodulin - Japan
44	223.5	25.7	149	2	I51402	calmodulin - Afric
45	223.5	25.7	149	2	S37707	calmodulin - mouse

#### ALIGNMENTS

##### RESULT 1

A33391

calcineurin regulatory chain - human

N;Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase chain B; protein phosphatase 2B

C;Species: Homo sapiens (man)

C;Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 09-Jul-2004

C;Accession: A33391

R;Guerini, D.; Krinks, M.H.; Sikela, J.M.; Hahn, W.E.; Klee, C.B.

DNA 8, 675-682, 1989

A;Title: Isolation and sequence of a cDNA clone for human calcineurin B, the Ca(2+)-binding subunit of the Ca(2+)/calmodulin-stimulated protein phosphatase.

A;Reference number: A33391; MUID:90126237; PMID:2558868

A;Accession: A33391

A;Molecule type: mRNA

A;Residues: 1-170 <GUE>

A;Cross-references: UNIPROT:P06705; GB:M30773; NID:g180704; PIDN:AAB08721.1; PID:g180705

C;Genetics:

A;Gene: GDB:PPP3R1; CALNB

A;Cross-references: GDB:136804; OMIM:601302  
A;Map position: 2p16-2p15  
C;Complex: heterodimer with calcineurin catalytic chain  
C;Superfamily: calmodulin; calmodulin repeat homology  
C;Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; lipoprotein; myristylation  
F;2-170/Product: calcineurin regulatory chain #status predicted <MAT>  
F;18-49/Domain: calmodulin repeat homology <EF1>  
F;50-82/Domain: calmodulin repeat homology <EF2>  
F;87-119/Domain: calmodulin repeat homology <EF3>  
F;128-160/Domain: calmodulin repeat homology <EF4>  
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted  
F;3/Modified site: aspartic acid (Asn) #status predicted  
F;31,33,35,37,42/Binding site: calcium (Asp, Asp, Ser, Ser, Glu) #status predicted  
F;63,65,67,69,74/Binding site: calcium (Asp, Asp, Asn, Glu, Glu) #status predicted  
F;100,102,104,106,111/Binding site: calcium (Asp, Asp, Asp, Tyr, Glu) #status predicted  
F;141,143,145,147,152/Binding site: calcium (Asp, Asp, Asp, Arg, Glu) #status predicted

Query Match 100.0%; Score 870; DB 1; Length 170;  
Best Local Similarity 100.0%; Pred. No. 6e-56;  
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 GNEASYPLEMC SHFDADEIKRLGKRFKKLDLDNSGSLSV EEFMSLP ELQQNPLVQRVIDI 60
          |||||||||||||||||||||||||||||||||||||||
Db      2 GNEASYPLEMC SHFDADEIKRLGKRFKKLDLDNSGSLSV EEFMSLP ELQQNPLVQRVIDI 61

Qy     61 FDTDGNGEVDFKEFIEGVSQFSVKGDKEQKLRFAFRIYDMDKDGYISNGELFQVLKMMVG 120
          |||||||||||||||||||||||||||||||||||||||
Db     62 FDTDGNGEVDFKEFIEGVSQFSVKGDKEQKLRFAFRIYDMDKDGYISNGELFQVLKMMVG 121

Qy    121 NNLKDTQLQQIVDKTIINADKDGGRISFEEFC AVVGGLDIHKKM VVDV 169
          |||||||||||||||||||||||||||||||||||
Db    122 NNLKDTQLQQIVDKTIINADKDGGRISFEEFC AVVGGLDIHKKM VVDV 170
```

## RESULT 2

S34127

calcineurin regulatory chain [validated] - bovine

N;Alternate names: calcineurin beta subunit; calcineurin chain B; phosphoprotein phosphatase chain B; protein phosphatase 2B

C;Species: Bos primigenius taurus (cattle)

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

C;Accession: I45831; JT0297; S34127

R;Nargang, C.E.; Bottorff, D.A.; Adachi, K.

DNA Seq. 4, 313-318, 1994

A;Title: Isolation and characterization of a cDNA clone coding for the calcium-binding subunit of calcineurin from bovine brain: an identical amino acid sequence to the human protein.

A;Reference number: I45831; MUID:95102111; PMID:7803816

A;Accession: I45831

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA



us-09-763-720-1.rup

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OM protein - protein search, using sw model

Run on: April 27, 2005, 09:07:47 ; Search time 175 Seconds  
(without alignments)  
494.522 Million cell updates/sec

Title: US-09-763-720-1  
Perfect score: 870  
Sequence: 1 GNEASYPLEMCSHFDADEIK.....EEFCVVGGLDIHKKMVDV 169

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	870	100.0	169	1	CALB_BOVIN	P63099 bos taurus
2	870	100.0	169	1	CALB_HUMAN	P63098 homo sapien
3	870	100.0	169	1	CALB_RAT	P63100 rattus norv
4	870	100.0	170	2	Q66HZ0	Q66hz0 brachydanio
5	870	100.0	170	2	Q6DJJ3	Q6djj3 xenopus lae
6	870	100.0	170	2	Q6VN50	Q6vn50 xenopus tro
7	870	100.0	170	2	Q6VN51	Q6vn51 gallus gall
8	865	99.4	169	1	CALB_MOUSE	Q63810 mus musculu
9	860	98.9	170	2	Q7T063	Q7t063 xenopus lae
10	795	91.4	765	2	Q86YQ0	Q86yq0 homo sapien
11	791	90.9	170	2	Q9NkW7	Q9nkw7 patinopecte
12	769	88.4	169	2	Q7PQ91	Q7pq91 anopheles g
13	766	88.0	170	1	CALC_DROME	Q24214 drosophila
14	762	87.6	170	1	CALB_DROME	P48451 drosophila
15	762	87.6	170	2	Q95P81	Q95p81 bombyx mori
16	734.5	84.4	169	2	Q86H16	Q86h16 schistosoma
17	733	84.3	169	1	CALC_HUMAN	Q961z3 homo sapien
18	732.5	84.2	169	2	Q9NFN1	Q9nfn1 schistosoma
19	707	81.3	170	2	Q7YRC9	Q7yrc9 macaca mula
20	704	80.9	171	2	Q20804	Q20804 caenorhabdi
21	702	80.7	178	1	CALC_MOUSE	Q63811 mus musculu

					us-09-763-720-1.rup	
22	699	80.3	175	1	CALC_RAT	P28470 rattus norv
23	580	66.7	115	2	Q99LQ9	Q99lq9 mus musculu
24	544	62.5	173	1	CALB_YARLI	Q6cge6 yarrowia li
25	540.5	62.1	174	1	CALB_NEUCR	P87072 neurospora
26	528	60.7	175	1	CALB_CRYNE	Q9hde1 cryptococcu
27	517	59.4	177	1	CALB_NAEGR	P42322 naegleria g
28	499	57.4	175	1	CALB_ASHGO	Q757b7 ashbya goss
29	496	57.0	174	1	CALB_YEAST	P25296 saccharomyc
30	483	55.5	174	1	CALB_SCHPO	Q9uu93 schizosacch
31	483	55.5	175	1	CALB_CANGA	Q6flu4 candida gla
32	475	54.6	175	1	CALB_KLULA	Q874t7 kluyveromyc
33	469	53.9	174	1	CALB_DEBHA	Q6bws8 debaryomyce
34	451	51.8	177	2	Q8MQT6	Q8mq6 toxoplasma
35	443.5	51.0	169	2	Q867N3	Q867n3 paramecium
36	442.5	50.9	180	2	Q9GP83	Q9gp83 dictyosteli
37	436	50.1	177	2	Q86RA7	Q86ra7 plasmodium
38	436	50.1	179	2	Q8IKV9	Q8ikv9 plasmodium
39	415.5	47.8	166	2	Q7RP38	Q7rp38 plasmodium
40	372	42.8	175	2	Q9U0X7	Q9u0x7 leishmania
41	340.5	39.1	194	1	CHP1_MOUSE	P61022 mus musculu
42	340.5	39.1	194	1	CHP1_RAT	P61023 rattus norv
43	338.5	38.9	193	2	Q6DK70	Q6dk70 xenopus tro
44	338.5	38.9	193	2	Q6DKL7	Q6dk17 xenopus lae
45	337.5	38.8	194	1	CHP1_HUMAN	Q99653 homo sapien

# ALIGNMENTS

## RESULT 1

### CALB\_BOVIN

ID CALB\_BOVIN STANDARD; PRT; 169 AA.  
AC P63099; P06705; P15117; Q08044;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory  
DE subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform  
DE 1).  
GN Name=PPP3R1; Synonyms=CNA2, CNB;  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=95102111; PubMed=7803816;  
RA Nargang C.E., Bottorff D.A., Adachi K.;  
RT "Isolation and characterization of a cDNA clone coding for the  
RT calcium-binding subunit of calcineurin from bovine brain: an identical  
RT amino acid sequence to the human protein.";  
RL DNA Seq. 4:313-318(1994).  
RN [2]  
RP SEQUENCE OF 1-168.  
RC TISSUE=Brain;  
RX MEDLINE=84132092; PubMed=6321184;  
RA Aitken A., Klee C.B., Cohen P.;  
RT "The structure of the B subunit of calcineurin.";  
RL Eur. J. Biochem. 139:663-671(1984).  
RN [3]  
RP CALCIUM-BINDING DATA.

us-09-763-720-1.rup

RX MEDLINE=80101597; PubMed=293720;  
RA Klee C.B., Crouch T.H., Krinks M.H.;  
RT "Calcineurin: a calcium- and calmodulin-binding protein of the nervous  
RT system.";  
RL Proc. Natl. Acad. Sci. U.S.A. 76:6270-6273(1979).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) IN COMPLEX WITH FKBP1A.  
RX MEDLINE=95360994; PubMed=7543369; DOI=10.1016/0092-8674(95)90439-5;  
RA Griffith J.P., Kim J.L., Kim E.E., Sintchak M.D., Thomson J.A.,  
RA Fitzgibbon M.J., Fleming M.A., Caron P.R., Hsiao K., Navia M.A.;  
RT "X-ray structure of calcineurin inhibited by the immunophilin-  
RT immunosuppressant FKBP12-FK506 complex.";  
RL Cell 82:507-522(1995).  
CC -!- FUNCTION: Regulatory subunit of calcineurin, a calcium-dependent,  
CC calmodulin stimulated protein phosphatase. Confers calcium  
CC sensitivity.  
CC -!- SUBUNIT: Composed of a catalytic subunit (A) and a regulatory  
CC subunit (B).  
CC -!- MISCELLANEOUS: This protein has four functional calcium-binding  
CC sites.  
CC -!- SIMILARITY: Contains 4 EF-hand calcium-binding domains.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; X71666; CAA50659.1; -.  
DR PIR; I45831; S34127.  
DR PDB; 1TCO; X-ray; B=1-169.  
DR GO; GO:0005955; C:calcineurin complex; NAS.  
DR GO; GO:0005509; F:calcium ion binding; NAS.  
DR GO; GO:0004723; F:calcium-dependent protein serine/threonine . . .; NAS.  
DR GO; GO:0005517; F:calmodulin inhibitor activity; NAS.  
DR InterPro; IPR002048; EF-hand.  
DR InterPro; IPR010983; EF\_Hand\_like.  
DR InterPro; IPR008080; Parvalbumin.  
DR InterPro; IPR001125; Recoverin.  
DR Pfam; PF00036; efhand; 4.  
DR PRINTS; PR01697; PARVALBUMIN.  
DR PRINTS; PR00450; RECOVERIN.  
DR PROSITE; PS00018; EF\_HAND; 4.  
KW 3D-structure; Calcium-binding; Direct protein sequencing; Lipoprotein;  
KW Myristate; Repeat.  
FT INIT\_MET 0 0  
FT LIPID 1 1 N-myristoyl glycine.  
FT CA\_BIND 30 41 EF-hand 1.  
FT CA\_BIND 62 73 EF-hand 2.  
FT CA\_BIND 99 110 EF-hand 3.  
FT CA\_BIND 140 151 EF-hand 4.  
FT CONFLICT 11 11 C -> M (in Ref. 2).  
FT CONFLICT 153 153 C -> S (in Ref. 2).  
FT HELIX 16 29  
FT TURN 31 32  
FT STRAND 36 37  
FT HELIX 39 42  
FT TURN 43 44  
FT HELIX 46 49  
FT TURN 50 50  
FT TURN 52 53

us-09-763-720-1.rup

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FT  HELIX      54      61
FT  TURN       63      64
FT  STRAND     69      70
FT  HELIX      71      78
FT  HELIX      79      81
FT  TURN       83      84
FT  HELIX      87      98
FT  TURN     100     101
FT  STRAND    105     106
FT  HELIX    108     119
FT  TURN    120     121
FT  HELIX    125     139
FT  TURN    141     142
FT  STRAND   147     148
FT  HELIX   149     156
FT  HELIX   157     159
FT  HELIX   161     164
SQ  SEQUENCE   169 AA;  19169 MW;  749141BD0434C90C CRC64;
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Query Match 100.0%; Score 870; DB 1; Length 169;  
Best Local Similarity 100.0%; Pred. No. 8.1e-52;  
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB     61 FDTDGNGEVDKFKEFIEGVSQFSVKGDKLRFQAFRIYDMKDGYSISNGELFQVLKMMVG 120

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DB    121 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGGLDIHKKMVVDV 169
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## RESULT 2

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ID CALB\_HUMAN STANDARD; PRT; 169 AA.  
AC P63098; P06705; P15117; Q08044;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory  
DE subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform  
DE 1).  
GN Name=PPP3R1; Synonyms=CNA2, CNB;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90126237; PubMed=2558868;  
RA Guerini D., Krinks M.H., Sikela J.M., Hahn W.E., Klee C.B.;  
RT "Isolation and sequence of a cDNA clone for human calcineurin B, the  
RT Ca<sup>2+</sup>-binding subunit of the Ca<sup>2+</sup>/calmodulin-stimulated protein  
RT phosphatase.";  
RL DNA 8:675-682(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;  
RT "Cloning of human full open reading frames in Gateway(TM) system entry

RT vector (pDONR201).";  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).  
 RX MEDLINE=96097077; PubMed=8524402; DOI=10.1038/378641a0;  
 RA Kissinger C.R., Parge H.E., Knighton D.R., Lewis C.T., Pelletier L.A.,  
 RA Tempczyk A., Kalish V.J., Tucker K.D., Showalter R.E., Moomaw E.W.,  
 RA Gastinel L.N., Habuka N., Chen X., Maldonado F., Barker J.E.,  
 RA Bacquet R., Villafranca J.E.;  
 RT "Crystal structures of human calcineurin and the human FKBP12-FK506-  
 RT calcineurin complex.";  
 RL Nature 378:641-644(1995).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) IN COMPLEX WITH PPIA.  
 RX PubMed=12218175; DOI=10.1073/pnas.192206699;  
 RA Huai Q., Kim H.Y., Liu Y., Zhao Y., Mondragon A., Liu J.O., Ke H.;  
 RT "Crystal structure of calcineurin-cyclophilin-cyclosporin shows common  
 RT but distinct recognition of immunophilin-drug complexes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:12037-12042(2002).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) IN COMPLEX WITH PPIA.  
 RX PubMed=12357034; DOI=10.1073/pnas.212504399;  
 RA Jin L., Harrison S.C.;  
 RT "Crystal structure of human calcineurin complexed with cyclosporin A  
 RT and human cyclophilin.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13522-13526(2002).  
 CC -!- FUNCTION: Regulatory subunit of calcineurin, a calcium-dependent,  
 CC calmodulin stimulated protein phosphatase. Confers calcium  
 CC sensitivity.  
 CC -!- SUBUNIT: Composed of a catalytic subunit (A) and a regulatory  
 CC subunit (B).  
 CC -!- MISCELLANEOUS: This protein has four functional calcium-binding  
 CC sites.  
 CC -!- SIMILARITY: Contains 4 EF-hand calcium-binding domains.  
 CC -----  
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 CC -----

DR EMBL; M30773; AAB08721.1; -.  
 DR EMBL; BC027913; AAH27913.1; -.  
 DR EMBL; CR456938; CAG33219.1; -.  
 DR PIR; A33391; A33391.  
 DR PDB; 1AUI; X-ray; B=1-169.  
 DR PDB; 1M63; X-ray; B/F=1-169.  
 DR PDB; 1MF8; X-ray; B=1-169.  
 DR OGP; P63098; -.  
 DR Genew; HGNC:9317; PPP3R1.  
 DR MIM; 601302; -.  
 DR GO; GO:0005955; C:calcineurin complex; NAS.  
 DR GO; GO:0005509; F:calcium ion binding; NAS.  
 DR GO; GO:0004723; F:calcium-dependent protein serine/threonine . . .; NAS.  
 DR GO; GO:0005517; F:calmodulin inhibitor activity; NAS.  
 DR InterPro; IPR002048; EF-hand.  
 DR InterPro; IPR010983; EF\_Hand\_like.  
 DR InterPro; IPR008080; Parvalbumin.  
 DR InterPro; IPR001125; Recoverin.  
 DR Pfam; PF00036; efhand; 4.  
 DR PRINTS; PR01697; PARVALBUMIN.  
 DR PRINTS; PR00450; RECOVERIN.  
 DR PROSITE; PS00018; EF\_HAND; 4.  
 KW 3D-structure; Calcium-binding; Lipoprotein; Myristate; Repeat.  
 FT INIT\_MET 0 0 By similarity.  
 FT LIPID 1 1 N-myristoyl glycine (By similarity).  
 FT CA\_BIND 30 41 EF-hand 1.  
 FT CA\_BIND 62 73 EF-hand 2.  
 FT CA\_BIND 99 110 EF-hand 3.  
 FT CA\_BIND 140 151 EF-hand 4.  
 FT HELIX 16 29  
 FT TURN 31 32  
 FT STRAND 36 37  
 FT HELIX 39 42  
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 FT STRAND 105 106  
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 FT HELIX 161 164  
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Query Match 100.0%; Score 870; DB 1; Length 169;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-52;  
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

us-09-763-720-1.rup

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Db      1 GNEASYPLEMCSHFDADEIKRLGKRFFKLDLDNSGSLSVVEEFMSLPQLQQNPLVQRVIDI 60

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Qy    121 NNLDKDTQLQQIVDKTIINADKGDGRISFEEFCAVVGGLDIHKKMVVDV 169
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Db    121 NNLDKDTQLQQIVDKTIINADKGDGRISFEEFCAVVGGLDIHKKMVVDV 169

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RESULT 3

CALB\_RAT

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ID  CALB_RAT      STANDARD;      PRT;    169 AA.
AC  P63100; P06705; P15117; Q08044;
DT  01-JAN-1988 (Rel. 06, Created)
DT  01-APR-1990 (Rel. 14, Last sequence update)
DT  25-OCT-2004 (Rel. 45, Last annotation update)
DE  Calcineurin B subunit isoform 1 (Protein phosphatase 2B regulatory
DE  subunit 1) (Protein phosphatase 3 regulatory subunit B alpha isoform
DE  1).
GN  Name=Ppp3r1; Synonyms=Cna2, Cnb;
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]
RP  SEQUENCE FROM N.A. (ISOFORM 1).
RC  STRAIN=Fischer;
RA  Perrino B.A., Huang X., Ng L.Y., Soderling T.R.;
RT  "Regulation of calcineurin phosphatase activity by the B subunit and
RT  carboxy-terminal inhibitory domains of the A subunit.";
RL  Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases.
RN  [2]
RP  SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.
RC  TISSUE=Brain, and Testis;
RX  MEDLINE=94153993; PubMed=8110831; DOI=10.1016/0167-4781(94)90031-0;
RA  Chang C.-D., Mukai H., Kuno T., Tanaka C.;
RT  "cDNA cloning of an alternatively spliced isoform of the regulatory
RT  subunit of Ca2+/calmodulin-dependent protein phosphatase (calcineurin
RT  B alpha 2).";
RL  Biochim. Biophys. Acta 1217:174-180(1994).
CC  -!- FUNCTION: Regulatory subunit of calcineurin, a calcium-dependent,
CC  calmodulin stimulated protein phosphatase. Confers calcium
CC  sensitivity.
CC  -!- SUBUNIT: Composed of a catalytic subunit (A) and a regulatory
CC  subunit (B).
CC  -!- ALTERNATIVE PRODUCTS:
CC  Event=Alternative splicing; Named isoforms=2;
CC  Name=1;
CC  IsoId=P63100-1, P06705-1;
CC  Sequence=Displayed;
CC  Name=2;
CC  IsoId=P63100-2, P06705-2;
CC  Sequence=VSP_000729;
CC  -!- TISSUE SPECIFICITY: Isoform 2 is testis specific.
CC  -!- MISCELLANEOUS: This protein has four functional calcium-binding
CC  sites.
CC  -!- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
CC  -----

```

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

Query Match 100.0%; Score 870; DB 1; Length 169;  
Best Local Similarity 100.0%; Pred. No. 8.1e-52;  
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	GNEASYPLEMCSHFDADAIKRLGKRFKKLDLDNSGSLSVEEFMSLP	60
Qy	61	FDTDGNGEVDFKEFIEGVSQFSVKGDKEQKLRF	120
Db	61	FDTDGNGEVDFKEFIEGVSQFSVKGDKEQKLRF	120
Qy	121	NNLKDTQLQQIVDKTIINADKDGGRISFEEFC	169
Db	121	NNLKDTQLQQIVDKTIINADKDGGRISFEEFC	169

Page 8



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                                us-09-763-720-1.rup
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole;
RX   PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole;
RA   Director MGC Project;
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC081617; AAH81617.1; -.
DR   InterPro; IPR001751; CaBP_S100.
DR   InterPro; IPR002048; EF-hand.
DR   InterPro; IPR010983; EF_Hand_like.
DR   InterPro; IPR008080; Parvalbumin.
DR   InterPro; IPR001125; Recoverin.
DR   Pfam; PF00036; efhand; 4.
DR   PRINTS; PR01697; PARVALBUMIN.
DR   PRINTS; PR00450; RECOVERIN.
DR   ProDom; PD003407; CaBP_S100; 1.
DR   ProDom; PD000012; EF-hand; 2.
DR   SMART; SM00054; EFh; 4.
DR   PROSITE; PS00018; EF_HAND; 4.
SQ   SEQUENCE 170 AA; 19300 MW; C904715DC0386056 CRC64;

Query Match 100.0%; Score 870; DB 2; Length 170;
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Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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db      2 GNEASYPLEMCSHFDADKRLGKRFKKLDLDNSGSLSVVEEFMSLPQLQNPLVQRVIDI 61

Qy      61 FDTDGNGEVDFKEFIEGVSVQSVKGDKEQKLRFARIYDMKDGYSNGELFQVLKMMVG 120
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Db 122 NNLKDTQLQQIVDKTIINADKDGDRISFEEFCAVVGGLDIHKKMVVDV 170

## RESULT 5

Q6DJJ3

ID Q6DJJ3 PRELIMINARY; PRT; 170 AA.

AC Q6DJJ3;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE MGC82148 protein.

GN Name=MGC82148;

OS *Xenopus laevis* (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipioidea; Pipidae;

OC Xenopodinae; *Xenopus*.

OX NCBI\_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;

RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,

RA Richardson P.;

RT "Genetic and genomic tools for *Xenopus* research: The NIH *Xenopus*

RT initiative.";

RL Dev. Dyn. 225:384-391(2002).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RA Klein S., Gerhard D.S.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC075185; AAH75185.1; -.

DR GO; GO:0005509; F:calcium ion binding; IEA.

DR InterPro; IPR001751; CaBP\_S100.

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR010983; EF\_Hand\_like.

DR InterPro; IPR008080; Parvalbumin.

DR InterPro; IPR001125; Recoverin.

DR Pfam; PF00036; efhand; 4.

```

DR PRINTS; PR01697; PARVALBUMIN.
DR PRINTS; PR00450; RECOVERIN.
DR ProDom; PD003407; CaBP_S100; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; 4.
KW Calcium; Calcium-binding.
SQ SEQUENCE 170 AA; 19300 MW; C904715DC0386056 CRC64;

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Query Match 100.0%; Score 870; DB 2; Length 170;  
Best Local Similarity 100.0%; Pred. No. 8.1e-52;  
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GNEASYPLEMCSHFDADEIKRLGKRFKKLDLNSGSLSVVEEFMSLPQLQQNPLVQRVIDI	60
Db	2	GNEASYPLEMCSHFDADEIKRLGKRFKKLDLNSGSLSVVEEFMSLPQLQQNPLVQRVIDI	61
Qy	61	FDTDGNGEVDKFKEFIEGVQSFSVKGDKEQKLRFARFYDMKDGYISNGELFQVLKMMVG	120
Db	62	FDTDGNGEVDKFKEFIEGVQSFSVKGDKEQKLRFARFYDMKDGYISNGELFQVLKMMVG	121
Qy	121	NNLKDTQLQQIVDKTIINADKDGGRISFEFCVVGGDIHKKMVVDV	169
Db	122	NNLKDTQLQQIVDKTIINADKDGGRISFEFCVVGGDIHKKMVVDV	170

**Q6VN50**

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Q6VN50      PRELIMINARY;          PRT;   170 AA.
AC      Q6VN50;
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT      25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE      Protein phosphatase 3 regulatory subunit B alpha isoform type 1
DE      (Hypothetical protein MGC75600).
GN      Name=MGC75600;
OS      Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC      Xenopodinae; Xenopus.
OX      NCBI_TaxID=8364;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Zhou G., Li W., Yu L., Zhao S.;
RL      Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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us-09-763-720-1.rup

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RA Klein S., Gerhard D.S.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AY336972; AAQ16148.1; -.  
DR EMBL; BC064854; AAH64854.1; -.  
DR HSSP; P02618; 1B8R.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR InterPro; IPR001751; CaBP\_S100.  
DR InterPro; IPR002048; EF-hand.  
DR InterPro; IPR010983; EF\_Hand\_like.  
DR InterPro; IPR008080; Parvalbumin.  
DR InterPro; IPR001125; Recoverin.  
DR Pfam; PF00036; efhand; 4.  
DR PRINTS; PR01697; PARVALBUMIN.  
DR PRINTS; PR00450; RECOVERIN.  
DR ProDom; PD003407; CaBP\_S100; 1.  
DR ProDom; PD000012; EF-hand; 2.  
DR SMART; SM00054; EFh; 4.  
DR PROSITE; PS00018; EF\_HAND; 4.  
KW Calcium; Calcium-binding; Hypothetical protein.  
SQ SEQUENCE 170 AA; 19300 MW; C904715DC0386056 CRC64;

Query Match 100.0%; Score 870; DB 2; Length 170;  
Best Local Similarity 100.0%; Pred. No. 8.1e-52;  
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

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Q6VN51

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Q6VN51      PRELIMINARY;      PRT;      170 AA.
AC      Q6VN51;
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      Protein phosphatase 3 regulatory subunit B alpha isoform type 1.
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Bursa;
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us-09-763-720-1.rup

RA Zhou G., Li W., Yu L., Zhao S.;  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY336970; AAQ16146.1; -.  
 DR HSSP; P02618; 1B8R.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR InterPro; IPR001751; CaBP\_S100.  
 DR InterPro; IPR002048; EF-hand.  
 DR InterPro; IPR010983; EF\_Hand\_like.  
 DR InterPro; IPR008080; Parvalbumin.  
 DR InterPro; IPR001125; Recoverin.  
 DR Pfam; PF00036; efhand; 4.  
 DR PRINTS; PR01697; PARVALBUMIN.  
 DR PRINTS; PR00450; RECOVERIN.  
 DR ProDom; PD003407; CaBP\_S100; 1.  
 DR ProDom; PD000012; EF-hand; 2.  
 DR SMART; SM00054; EFh; 4.  
 DR PROSITE; PS00018; EF\_HAND; 4.  
 KW Calcium; Calcium-binding.  
 SQ SEQUENCE 170 AA; 19300 MW; C904715DC0386056 CRC64;

Query Match 100.0%; Score 870; DB 2; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-52;  
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	2	GNEASYPLEMCSHFD	AEIKRLGKR	FKKLDLDNSG	SLVVEEFMSL	PELQQNPLVQR	VIDI	61
Qy	61	FDTDGN	GEVDFKEF	IEGVSQFSV	KDKEQKL	RFAFRIYD	MDKDG	120
Db	62	FDTDGN	GEVDFKEF	IEGVSQFSV	KDKEQKL	RFAFRIYD	MDKDG	121
Qy	121	NNLKDTQL	QQIVDKTI	INADKDG	DGRISFEE	FCAVVGGL	DIHKM	169
Db	122	NNLKDTQL	QQIVDKTI	INADKDG	DGRISFEE	FCAVVGGL	DIHKM	170

us-09-763-720-1.rapb

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 27, 2005, 09:03:38 ; Search time 51 Seconds  
(without alignments)  
1102.778 Million cell updates/sec

Title: US-09-763-720-1  
Perfect score: 870  
Sequence: 1 GNEASYPLEMCSHFDADK.....EEFCAVVGGLDIHKMVDV 169

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
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13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	870	100.0	170	13	US-10-109-885-3	Sequence 3, Appli
2	870	100.0	170	14	US-10-309-280-3	Sequence 3, Appli
3	733	84.3	170	15	US-10-239-572-2	Sequence 2, Appli

us-09-763-720-1.rapb					
4	733	84.3	173	15 US-10-094-749-3200	Sequence 3200, Ap
5	733	84.3	187	11 US-09-764-875-845	Sequence 845, App
6	733	84.3	189	9 US-09-764-881-148	Sequence 148, App
7	733	84.3	189	10 US-09-764-891-3897	Sequence 3897, Ap
8	733	84.3	189	10 US-09-764-881-148	Sequence 148, App
9	733	84.3	189	11 US-09-764-875-1133	Sequence 1133, Ap
10	733	84.3	189	15 US-10-242-747-148	Sequence 148, App
11	733	84.3	189	15 US-10-158-057-242	Sequence 242, App
12	733	84.3	189	15 US-10-158-057-317	Sequence 317, App
13	501	57.6	197	15 US-10-369-493-13106	Sequence 13106, A
14	496	57.0	175	15 US-10-369-493-22220	Sequence 22220, A
15	429.5	49.4	195	15 US-10-369-493-22782	Sequence 22782, A
16	429	49.3	185	15 US-10-369-493-4075	Sequence 4075, Ap
17	373.5	42.9	178	14 US-10-342-224-54	Sequence 54, Appl
18	340.5	39.1	195	9 US-09-999-602-3	Sequence 3, Appli
19	340.5	39.1	195	17 US-10-482-838-18	Sequence 18, Appl
20	337.5	38.8	194	17 US-10-480-847-6	Sequence 6, Appli
21	337.5	38.8	195	9 US-09-999-602-4	Sequence 4, Appli
22	337.5	38.8	195	17 US-10-482-838-17	Sequence 17, Appl
23	316.5	36.4	213	15 US-10-369-493-6287	Sequence 6287, Ap
24	303.5	34.9	195	15 US-10-369-493-6454	Sequence 6454, Ap
25	292	33.6	207	9 US-09-764-881-145	Sequence 145, App
26	292	33.6	207	10 US-09-764-881-145	Sequence 145, App
27	292	33.6	207	11 US-09-764-875-1138	Sequence 1138, Ap
28	292	33.6	207	15 US-10-242-747-145	Sequence 145, App
29	292	33.6	207	15 US-10-158-057-320	Sequence 320, App
30	291	33.4	196	17 US-10-482-838-9	Sequence 9, Appli
31	291	33.4	210	11 US-09-764-875-854	Sequence 854, App
32	289	33.2	199	15 US-10-276-774-2317	Sequence 2317, Ap
33	284	32.6	194	16 US-10-322-281-506	Sequence 506, App
34	280	32.2	196	17 US-10-482-838-16	Sequence 16, Appl
35	248	28.5	175	15 US-10-424-599-185489	Sequence 185489,
36	240	27.6	208	15 US-10-425-114-57256	Sequence 57256, A
37	233	26.8	194	15 US-10-425-114-65892	Sequence 65892, A
38	231.5	26.6	218	15 US-10-425-114-47771	Sequence 47771, A
39	230.5	26.5	171	16 US-10-437-963-185345	Sequence 185345,
40	230.5	26.5	174	15 US-10-425-114-59559	Sequence 59559, A
41	230.5	26.5	181	15 US-10-425-114-46972	Sequence 46972, A
42	230.5	26.5	183	15 US-10-425-114-44959	Sequence 44959, A
43	230.5	26.5	183	15 US-10-425-114-56162	Sequence 56162, A
44	230.5	26.5	183	15 US-10-425-114-60654	Sequence 60654, A
45	230.5	26.5	184	15 US-10-425-114-56165	Sequence 56165, A

#### ALIGNMENTS

#### RESULT 1

US-10-109-885-3

; Sequence 3, Application US/10109885

; Publication No. US20020119129A1

; GENERAL INFORMATION:

; APPLICANT: REVEL, Michel

; APPLICANT: CHEBATH, Judith

; APPLICANT: ABRAMOVITCH, Carolina

; TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND

METHODS OF

; TITLE OF INVENTION: MODULATING CELLULAR RESPONSE TO INTERFERON

; FILE REFERENCE: REVEL=14A

; CURRENT APPLICATION NUMBER: US/10/109,885

; CURRENT FILING DATE: 2002-04-01

; PRIOR APPLICATION NUMBER: US/09/341,640

; PRIOR FILING DATE: 1999-10-18

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; us-09-763-720-1.rapb
; PRIOR APPLICATION NUMBER: PCT/US98/00671
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: US 60/035,636
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic
US-10-109-885-3

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Best Local Similarity 100.0%; Pred. No. 2.4e-74;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 FDTDGNGEVDFKEFIEGVSVQFSVKGDKKEQKLRFARIYDMDKDGYISNGELFQVLKMMVG 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 FDTDGNGEVDFKEFIEGVSVQFSVKGDKKEQKLRFARIYDMDKDGYISNGELFQVLKMMVG 121

Qy    121 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGLDIHKKMVVDV 169
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 2
US-10-309-280-3
; Sequence 3, Application US/10309280
; Publication No. US20030176678A1
; GENERAL INFORMATION:
;   APPLICANT: REVEL, Michel
;   APPLICANT: CHEBATH, Judith
;   APPLICANT: ABRAMOVITCH, Carolina
;   TITLE OF INVENTION: NOVEL IFN RECEPTOR I BINDING PROTEIN, DNA ENCODING THEM, AND
METHODS OF
;   TITLE OF INVENTION: MODULATING CELLULAR RESPONSE TO INTERFERON
;   FILE REFERENCE: REVEL=14A
;   CURRENT APPLICATION NUMBER: US/10/309,280
;   CURRENT FILING DATE: 2002-12-04
;   PRIOR APPLICATION NUMBER: US/09/341,640
;   PRIOR FILING DATE: 1999-10-18
;   PRIOR APPLICATION NUMBER: PCT/US98/00671
;   PRIOR FILING DATE: 1998-01-15
;   PRIOR APPLICATION NUMBER: US 60/035,636
;   PRIOR FILING DATE: 1997-01-15
;   NUMBER OF SEQ ID NOS: 13
;   SOFTWARE: PatentIn version 3.1
;   SEQ ID NO 3
;   LENGTH: 170
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic
US-10-309-280-3

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Query Match          100.0%; Score 870; DB 14; Length 170;
Best Local Similarity 100.0%; Pred. No. 2.4e-74;

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us-09-763-720-1.rapb

Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 FDTDGNGEVDKFKEFIEGVSQFSVKGDKLRFQAFRIYDMDKDGYSNGELFQVLKMMVG 120
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Db     62 FDTDGNGEVDKFKEFIEGVSQFSVKGDKLRFQAFRIYDMDKDGYSNGELFQVLKMMVG 121

Qy    121>NNLKDTQLQQIVDKTIINADKDGGRISFEEFCAVVGGLDIHKKMVVDV 169
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122>NNLKDTQLQQIVDKTIINADKDGGRISFEEFCAVVGGLDIHKKMVVDV 170
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A;Residues: 1-170 <NA2>  
A;Cross-references: UNIPROT:P06705; EMBL:X71666; NID:g312968; PIDN:CAA50659.1; PID:g312969  
R;Aitken, A.; Klee, C.B.; Cohen, P.  
Eur. J. Biochem. 139, 663-671, 1984  
A;Title: The structure of the B-subunit of calcineurin.  
A;Reference number: JT0297; MUID:84132092; PMID:6321184  
A;Accession: JT0297  
A;Molecule type: protein  
A;Residues: 2-11,'M',13-153,'S',155-169 <AIT>  
R;Griffith, J.P.; Kim, J.L.; Kim, E.E.; Sintchak, M.D.; Thomson, J.A.; Fitzgibbon, M.J.; Fleming, M.A.; Caron, P.R.; Hsiao, K.; Navia, M.A.  
submitted to the Brookhaven Protein Data Bank, August 1996  
A;Reference number: A66708; PDB:1TCO  
A;Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 2-170  
R;Griffith, J.P.; Kim, J.L.; Kim, E.E.; Sintchak, M.D.; Thomson, J.A.; Fitzgibbon, M.J.; Fleming, M.A.; Caron, P.R.; Hsiao, K.; Navia, M.A.  
Cell 82, 507-522, 1995  
A;Title: X-ray structure of calcineurin inhibited by the immunophilin-immunosuppressant FKBP12-FK506 complex.  
A;Reference number: A56967; MUID:95360994; PMID:7543369  
A;Contents: annotation; X-ray crystallography, 2.5 angstroms  
C;Complex: heterodimer with calcineurin catalytic chain (see PIR:A56968)  
C;Superfamily: calmodulin; calmodulin repeat homology  
C;Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; lipoprotein; myristylation  
F;2-170/Product: calcineurin regulatory chain #status experimental <MAT>  
F;18-49/Domain: calmodulin repeat homology <EF1>  
F;50-82/Domain: calmodulin repeat homology <EF2>  
F;87-119/Domain: calmodulin repeat homology <EF3>  
F;128-160/Domain: calmodulin repeat homology <EF4>  
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status experimental  
F;3/Modified site: aspartic acid (Asn) #status predicted  
F;31,33,35,37,42/Binding site: calcium (Asp, Asp, Ser, Ser, Glu) #status experimental  
F;63,65,67,69,74/Binding site: calcium (Asp, Asp, Asn, Glu, Glu) #status experimental  
F;100,102,104,106,111/Binding site: calcium (Asp, Asp, Asp, Tyr, Glu) #status experimental  
F;141,143,145,147,152/Binding site: calcium (Asp, Asp, Asp, Arg, Glu) #status experimental

Query Match 100.0%; Score 870; DB 1; Length 170;  
Best Local Similarity 100.0%; Pred. No. 6e-56;  
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GNEASYPLEMCSHFDADEIKRLGKRFKKLDLDNSGSLSVEEFMSLPQLQONPLVQRVIDI 60
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Db      2 GNEASYPLEMCSHFDADEIKRLGKRFKKLDLDNSGSLSVEEFMSLPQLQONPLVQRVIDI 61

Qy     61 FDTDGNGEVDFKEFIEGVSQFSVKGDKQKLRFAFRIYDMKDGYSISNGELFQVLKMMVG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 FDTDGNGEVDFKEFIEGVSQFSVKGDKQKLRFAFRIYDMKDGYSISNGELFQVLKMMVG 121

Qy    121 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGGLDIHKKMVVDV 169
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```



Db 108 FDTDGNGEVDFKEFIEGVSVQFSVKGDKQKLRFAFRIYDMDKDGYSISNGELFQVLKMMVG 167

Qy 121 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGLDIHKKMVVDV 169  
 |||

Db 168 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGLDIHKKMVVDV 216

# RESULT 4

JC1220

calcineurin regulatory chain, brain - mouse

N;Alternate names: calcineurin beta-1 subunit; calcineurin chain B-1;

phosphoprotein phosphatase chain B; protein phosphatase 2B

C;Species: Mus musculus (house mouse)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C;Accession: JC1220

R;Ueki, K.; Muramatsu, T.; Kincaid, R.L.

Biochem. Biophys. Res. Commun. 187, 537-543, 1992

A;Title: Structure and expression of two isoforms of the murine calmodulin-dependent protein phosphatase regulatory subunit (calcineurin B).

A;Reference number: JC1220; MUID:92392379; PMID:1325794

A;Accession: JC1220

A;Molecule type: mRNA

A;Residues: 1-170 <UEK>

A;Cross-references: UNIPROT:Q63810; GB:S43864; NID:g255078; PIDN:AAB23171.1; PID:g255079

A;Experimental source: brain

C;Comment: With calcineurin catalytic chain plays an important role in neural and nonneural calcium-regulated signaling.

C;Genetics:

A;Gene: PP2B-beta-1

C;Complex: heterodimer with calcineurin catalytic chain

C;Superfamily: calmodulin; calmodulin repeat homology

C;Keywords: blocked amino end; calcium binding; duplication; EF hand; heterodimer; lipoprotein; myristylation

F;2-170/Product: calcineurin regulatory chain #status predicted <MAT>

F;18-49/Domain: calmodulin repeat homology <EF1>

F;50-82/Domain: calmodulin repeat homology <EF2>

F;87-119/Domain: calmodulin repeat homology <EF3>

F;128-160/Domain: calmodulin repeat homology <EF4>

F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

Query Match 99.4%; Score 865; DB 1; Length 170;

Best Local Similarity 99.4%; Pred. No. 1.4e-55;

Matches 168; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GNEASYPLEMCSHFDADEIKRLGKRFKKLDLDNSGSLSVEEFMSLPELQQNPLVQRVIDI 60  
 |:|

Db 2 GSEASYPLEMCSHFDADEIKRLGKRFKKLDLDNSGSLSVEEFMSLPELQQNPLVQRVIDI 61

Qy 61 FDTDGNGEVDFKEFIEGVSVQFSVKGDKQKLRFAFRIYDMDKDGYSISNGELFQVLKMMVG 120  
 |||

Db 62 FDTDGNGEVDFKEFIEGVSVQFSVKGDKQKLRFAFRIYDMDKDGYSISNGELFQVLKMMVG 121

Qy 121 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGLDIHKKMVVDV 169  
 |||

Db 122 NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGLDIHKKMVVDV 170

us-09-763-720-1.ra1

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 27, 2005, 09:03:38 ; Search time 22 Seconds  
(without alignments)  
573.441 Million cell updates/sec

Title: US-09-763-720-1  
Perfect score: 870  
Sequence: 1 GNEASYPLEMCSHFDADEIK.....EEFCAVVGGLDIHKKMVVDV 169

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	870	100.0	169	3	US-08-720-625-4	Sequence 4, Appli
2	870	100.0	170	3	US-08-764-563-5	Sequence 5, Appli
3	702	80.7	179	3	US-08-764-563-4	Sequence 4, Appli
4	517	59.4	177	3	US-08-764-563-3	Sequence 3, Appli
5	496	57.0	174	1	US-08-328-322-17	Sequence 17, Appl
6	488	56.1	157	1	US-08-328-322-15	Sequence 15, Appl
7	469	53.9	204	4	US-09-248-796A-18332	Sequence 18332, A
8	393	45.2	90	4	US-09-513-999C-7071	Sequence 7071, Ap
9	321.5	37.0	233	4	US-09-270-767-42765	Sequence 42765, A
10	284	32.6	196	3	US-09-048-889-1	Sequence 1, Appli
11	242.5	27.9	145	3	US-08-720-625-5	Sequence 5, Appli
12	233.5	26.8	150	3	US-09-239-909-4	Sequence 4, Appli
13	225.5	25.9	149	3	US-08-963-409-3	Sequence 3, Appli
14	223.5	25.7	149	3	US-08-963-409-4	Sequence 4, Appli
15	223.5	25.7	149	3	US-08-641-873-20	Sequence 20, Appl
16	223.5	25.7	149	4	US-09-513-999C-7913	Sequence 7913, Ap
17	223.5	25.7	149	4	US-09-949-016-6770	Sequence 6770, Ap

				us-09-763-720-1.ra		
18	223.5	25.7	184	4	US-09-949-016-7507	Sequence 7507, Ap
19	222.5	25.6	416	4	US-09-989-025A-8	Sequence 8, Appli
20	221.5	25.5	150	3	US-09-239-909-2	Sequence 2, Appli
21	220.5	25.3	148	4	US-09-989-025A-4	Sequence 4, Appli
22	220.5	25.3	187	4	US-09-949-016-6721	Sequence 6721, Ap
23	215.5	24.8	142	1	US-07-951-715A-24	Sequence 24, Appl
24	215.5	24.8	142	2	US-08-459-448A-24	Sequence 24, Appl
25	215.5	24.8	142	3	US-08-459-595A-24	Sequence 24, Appl
26	215.5	24.8	142	3	US-08-459-504B-24	Sequence 24, Appl
27	215.5	24.8	142	3	US-08-459-444-24	Sequence 24, Appl
28	215.5	24.8	142	3	US-09-547-422-24	Sequence 24, Appl
29	215.5	24.8	142	4	US-09-988-462-24	Sequence 24, Appl
30	215	24.7	642	2	US-08-818-253-2	Sequence 2, Appli
31	215	24.7	642	3	US-08-818-252-2	Sequence 2, Appli
32	215	24.7	652	2	US-08-818-253-4	Sequence 4, Appli
33	215	24.7	652	3	US-08-818-252-4	Sequence 4, Appli
34	212	24.4	152	3	US-08-963-409-5	Sequence 5, Appli
35	212	24.4	152	4	US-09-949-016-6600	Sequence 6600, Ap
36	212	24.4	642	2	US-08-818-253-6	Sequence 6, Appli
37	212	24.4	642	3	US-08-818-252-6	Sequence 6, Appli
38	212	24.4	656	2	US-08-818-253-8	Sequence 8, Appli
39	212	24.4	656	3	US-08-818-252-8	Sequence 8, Appli
40	206.5	23.7	149	1	US-08-100-874-2	Sequence 2, Appli
41	205	23.6	100	4	US-09-270-767-46741	Sequence 46741, A
42	205	23.6	163	2	US-08-698-805-8	Sequence 8, Appli
43	204.5	23.5	408	1	US-07-951-715A-21	Sequence 21, Appl
44	204.5	23.5	408	2	US-08-459-448A-21	Sequence 21, Appl
45	204.5	23.5	408	3	US-08-459-595A-21	Sequence 21, Appl

#### ALIGNMENTS

#### RESULT 1

US-08-720-625-4

; Sequence 4, Application US/08720625

; Patent No. 6242587

; GENERAL INFORMATION:

; APPLICANT: Naik, Ulhas P.

; APPLICANT: Parise, Leslie V.

; TITLE OF INVENTION: CALCIUM-INTEGRIN BINDING PROTEIN

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Bell, Seltzer, Park & Gibson

; STREET: P.O. Drawer 34009

; CITY: Charlotte

; STATE: No. 6242587th Carolina

; COUNTRY: USA

; ZIP: 28234

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/720,625

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Sibley, Kenneth D.

; REGISTRATION NUMBER: 31,665

; REFERENCE/DOCKET NUMBER: 5470-138

; TELECOMMUNICATION INFORMATION:

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us-09-763-720-1.ra
: TELEPHONE: 919-420-2200
: TELEFAX: 919-881-3175
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 169 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-720-625-4

Query Match          100.0%; Score 870; DB 3; Length 169;
Best Local Similarity 100.0%; Pred. No. 5.1e-81;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GNEASYPLEMCSHFDADAIEKRLGKRFKKLDLDNSGSLSVEEFMSPPELQQNPLVQRVIDI 60
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Db      1 GNEASYPLEMCSHFDADAIEKRLGKRFKKLDLDNSGSLSVEEFMSPPELQQNPLVQRVIDI 60

Qy      61 FDTDGNGEVDFKEFIEGVSVQFSVKGDKQKLRFAFRIYDMDKDGYISNGELFQVLKMMVG 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 FDTDGNGEVDFKEFIEGVSVQFSVKGDKQKLRFAFRIYDMDKDGYISNGELFQVLKMMVG 120

Qy      121 NNLKDTQLQQIVDKTIINADKDGGRISFEFCAVVGGLDIHKKMVVDV 169
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 NNLKDTQLQQIVDKTIINADKDGGRISFEFCAVVGGLDIHKKMVVDV 169

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```

RESULT 2
US-08-764-563-5
: Sequence 5, Application US/08764563
: Patent No. 6093565
: GENERAL INFORMATION:
: APPLICANT: Hillman, Jennifer L.
: APPLICANT: Goli, Surya K.
: TITLE OF INVENTION: A NOVEL PROTEIN PHOSPHATASE
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/764,563
: FILING DATE: Herewith
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0178 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-855-0555
: TELEFAX: 415-845-4166

```

us-09-763-720-1.ra1

; TELEX:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 170 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 461682  
; US-08-764-563-5

Query Match 100.0%; Score 870; DB 3; Length 170;  
Best Local Similarity 100.0%; Pred. No. 5.1e-81;  
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GNEASYPLEMCSHFDADEIKRLGKRFKKLDLNSGSLSVEEFMSLP	60
Db	2	GNEASYPLEMCSHFDADEIKRLGKRFKKLDLNSGSLSVEEFMSLP	61
Qy	61	FDTDGNGEVDFKEFIEGVSQFSVKGDKLRFQVLRVIDI	120
Db	62	FDTDGNGEVDFKEFIEGVSQFSVKGDKLRFQVLRVIDI	121
Qy	121	NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGGLDIHKKMVVDV	169
Db	122	NNLKDTQLQQIVDKTIINADKDGGRISFEEFCVVGGGLDIHKKMVVDV	170